

Dietmar Spengler and Laurent Journot
Serial No.: 09/254,870
Filed: August 16, 1999
Page 2

comply with the Sequence Rules and that applicants must provide
1) a substitute computer readable form (CRF) copy of the
"Sequence Listing"; 2) a substitute paper copy of the "Sequence
Listing ", as well as an amendment directing its entry into the
specification; AND 3) a statement that the content of the paper
and computer readable copies are the same and, where applicable,
include no new matter, as required by 37 C.F.R. §1.821(e) or
§1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

Please amend the specification as follows:

In the Specification

Please delete the previously submitted paper copy of the
"Sequence Listing" inserted after page 71.

Please insert after page 71 the amended paper copy of the
"Sequence Listing", attached to hereto as **Exhibit B**.

REMARKS

In response to the May 24, 2000 Notice, applicants submit
herewith a computer readable form (CRF) copy of a revised
Sequence Listing which is set forth on the newly submitted paper
copy of revised Sequence Listing.

Applicants further submit a paper copy of the revised Sequence
Listing, attached hereto as **Exhibit B**, and a Statement in
Accordance with 37 C.F.R. §1.821(f), attached hereto as **Exhibit
C**, certifying that the computer readable form as required by 37
C.F.R. §1.821(e) is identical to the paper copy of Sequence

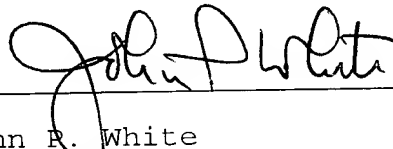
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Listing.

Applicants are submitting herewith a computer diskette containing
a C.F.R. of the sequence listing.

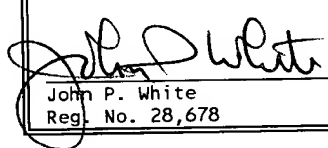
No fee is deemed necessary in connection with the filing of this
Amendment. However, if any fee is required, authorization is
hereby given to charge the amount of any such fee to Deposit
Account No. 03-3125.

Respectfully submitted,



John P. White
Registration No. 28,678
Attorney for Applicants
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

I hereby certify that this correspondence
is being deposited this date with the U.S.
Postal Service with sufficient postage as
first class mail addressed to: Assistant
Commissioner for Patents and Trademarks,
Washington, D.C. 20231.

 John P. White
Reg. No. 28,678

Date

6/26/00



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DEA/FCE-1994

| SERIAL NUMBER | FILING DATE | FIRST NAMED APPLICANT | ATTORNEY DOCKET NO. |
|---------------|-------------|-----------------------|---------------------|
| | | | |

| EXAMINER | |
|----------|--------------|
| | |
| ART UNIT | PAPER NUMBER |
| | 7 |

DATE MAILED: 5/24/00

1mo: 6/24/00

6mo: 11/24/00 W.D

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents
This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 because applicant has not submitted a CRF.

APPLICANT IS GIVEN ONE MONTH, or THIRTY DAYS, WHICHEVER IS LONGER FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for response beyond the SIX MONTH statutory period. Direct the response to the undersigned.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Charles L. Patterson, Jr., Ph.D. whose telephone number is (703) 308-1834. The examiner can normally be reached on any day of the week from 7:30 AM until 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy, can be reached on (703) 308-3804. The fax phone number for this Group is (703) 305-7401.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Patterson
May 18, 2000

CHARLES L. PATTERSON, JR.
PRIMARY EXAMINER
GROUP 1800



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Foerderung der
Wissenschaften e.V.
(B) STREET: none
(C) CITY: Berlin
(E) COUNTRY: DE
(F) POSTAL CODE (ZIP): none

- (A) NAME: CNRS
(B) STREET: rue de la cardonille
(C) CITY: Montpellier Cedex 05
(E) COUNTRY: FR
(F) POSTAL CODE (ZIP): 34094

(ii) TITLE OF INVENTION: Nucleic acid molecules coding for mammalian
tumor suppressor proteins and methods for their isolation

(iii) NUMBER OF SEQUENCES: 17

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 542..2545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCGGGA GAGCAAGCGG GCATCTCCTG GGCGCCGTCA TGGCTGCTTA GGCTGCGCTG 60
CCTGCGGATC GCGGATCCGG GATCGGAGAT CTGACGGCGA CGCCTGAGTC CGGCTAGGGT 120
AGGTCTGGGT TGGAGTCTGT GCCTGCTTCC TTGGCGTGTG GTTGTTCTCTG CTTGATTGCT 180
TCAGCGTGCC ATCGGCTTCG TATTTGCATA GGAGTCAGAG GAGTTAATCT TGTCTCCTCG 240
AAGATAGACT CTCATGGTTT ATGATCCATC TCTGTGAGAA GACTTTATTT GTCTGTCTCT 300

| | |
|---|------|
| TCTCACAGGT TTGAGTCTTC AGACTTCTAC AGAACTCCAT AATATCTGCC TCACAGCTGG | 360 |
| CTTTCCTGCT CTCACAGAAG ATACCCAGCT ATTGTGCTCT GGATCTCTCC TGGCTGCTAG | 420 |
| GCTGTAGCGC TGCCTTTCTG GAGTCAGGCT GTAGTGACTC CCCACCTTCT TTCTGTCTGG | 480 |
| GCTTAAATGG CACAGCAGTT CCTCAGCACA TCTGAAGAAG AAAGTGTGAG AACCAAAGGC | 540 |
| C ATG GCT CCA TTC CGC TGT CAA AAA TGT GGC AAG TCC TTC GTC ACC | 586 |
| Met Ala Pro Phe Arg Cys Gln Lys Cys Gly Lys Ser Phe Val Thr | |
| 1 5 10 15 | |
| CTG GAG AAG TTC ACC ATT CAC AAT TAT TCC CAC TCC AGG GAG CGC CCA | 634 |
| Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro | |
| 20 25 30 | |
| TTC AAG TGC TCG AAG GCT GAG TGT GGC AAA GCC TTC GTC TCC AAG TAT | 682 |
| Phe Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr | |
| 35 40 45 | |
| AAG CTG ATG AGA CAC ATG GCC ACA CAC TCG CCA CAG AAG ATT CAC CAG | 730 |
| Lys Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln | |
| 50 55 60 | |
| TGT ACT CAC TGT GAG AAG ACA TTC AAC CGG AAG GAC CAC CTG AAG AAC | 778 |
| Cys Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn | |
| 65 70 75 | |
| CAC CTC CAG ACC CAC GAT CCC AAC AAG ATC TCC TAC GCG TGT GAC GAT | 826 |
| His Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp | |
| 80 85 90 95 | |
| TGC GGC AAG AAG TAC CAC ACC ATG CTG GGC TAC AAG AGG CAC CTG GCC | 874 |
| Cys Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala | |
| 100 105 110 | |
| CTG CAC TCG GCG AGC AAT GGC GAT CTC ACC TGT GGG GTG TGC ACC CTG | 922 |
| Leu His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu | |
| 115 120 125 | |
| GAG CTG GGG AGC ACC GAG GTC CTG CTG GAC CAC CTC AAG TCT CAC GCG | 970 |
| Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala | |
| 130 135 140 | |
| GAA GAA AAG GCC AAC CAG GCA CCC AGG GAG AAG AAA TAC CAG TGC GAC | 1018 |
| Glu Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp | |
| 145 150 155 | |
| CAC TGT GAT AGA TGC TTC TAC ACC CGG AAA GAT GTG CGT CGC CAC CTG | 1066 |
| His Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg-His Leu | |
| 160 165 170 175 | |
| GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGT CAG TTC TGT GCC CAG | 1114 |
| Val Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln | |
| 180 185 190 | |
| AGA TTT GGG CGC AAA GAC CAC CTC ACT CGT CAC ACC AAG AAG ACC CAC | 1162 |
| Arg Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His | |
| 195 200 205 | |

| | |
|---|------|
| TCC CAG GAG CTG ATG CAA GAG AAT ATG CAG GCA GGA GAT TAC CAG AGC Ser Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser 210 215 220 | 1210 |
| AAT TTC CAA CTC ATT GCG CCT TCA ACT TCG TTC CAG ATA AAG GTT GAT Asn Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp 225 230 235 | 1258 |
| CCC ATG CCT CCT TTC CAG CTA GGA GCG GCT CCC GAG AAC GGG CTT GAT Pro Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp 240 245 250 255 | 1306 |
| GGT GGC TTG CCA CCC GAG GTT CAT GGT CTA GTG CTT GCT GCC CCA GAA Gly Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu 260 265 270 | 1354 |
| GAA GCT CCC CAA CCC ATG CCG CCC TTG GAG CCT TTG GAG CCT TTG GAG Glu Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu 275 280 285 | 1402 |
| CCT TTG GAG CCT TTG GAG CCG ATG CAG TCT TTG GAG CCT TTG CAG CCT Pro Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro 290 295 300 | 1450 |
| TTG GAG CCG ATG CAG CCT TTG GAG CCA ATG CAG CCT TTG GAG CCG ATG Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met 305 310 315 | 1498 |
| CAG CCT TTA GAG CCT TTG GAG CCT CTG GAG CCG ATG CAG CCT TTG GAG Gln Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu 320 325 330 335 | 1546 |
| CCG ATG CAG CCT TTG GAG CCT ATG CAG CCA ATG CTG CCA ATG CAG CCA Pro Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro 340 345 350 | 1594 |
| ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CAG CCA ATG Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met 355 360 365 | 1642 |
| CTG CCA ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CCA Leu Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro 370 375 380 | 1690 |
| GAG CCG TCT TTC ACT CTG CAC CCT GGC GTA GTT CCC ACC TCT CCT CCC Glu Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro 385 390 395 | 1738 |
| CCA ATT ATT CTT CAG GAG CAT AAG TAT AAT CCT GTT CCT ACC TCA TAT Pro Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr 400 405 410 415 | 1786 |
| GCC CCA TTT GTA GGC ATG CCC GTC AAA GCA GAT GGC AAG GCC TTT TGC Ala Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys 420 425 430 | 1834 |
| AAC GTG GGT TTC TTT GAG GAA TTT CCT CTG CAA GAG CCT CAG GCG CCT Asn Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro | 1882 |

| 435 | 440 | 445 | |
|---|-----|-----|------|
| CTC AAG TTC AAC CCA TGT TTT GAG ATG CCT ATG GAG GGG TTT GGG AAA Leu Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys 450 455 460 | | | 1930 |
| GTC ACC CTG TCC AAA GAG CTG CTG GTA GAT GCT GTG AAT ATA GCC ATT Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile 465 470 475 | | | 1978 |
| CCT GCC TCT CTG GAG ATT TCC TCC CTA TTG GGG TTT TGG CAG CTC CCC Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro 480 485 490 495 | | | 2026 |
| CCT CCT ACT CCC CAG AAT GGC TTT GTG AAT AGC ACC ATC CCT GTG GGG Pro Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly 500 505 510 | | | 2074 |
| CCT GGG GAG CCA CTG CCC CAT AGG ATA ACC TGT CTG GCG CAG CAG CAG Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln 515 520 525 | | | 2122 |
| CCA CCG CCA CTG CCG CCG CCA CCA CCG CTG CCA CTG CCA CAG CCA CTG Pro Pro Pro Leu Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu 530 535 540 | | | 2170 |
| CCA GTG CCA CAG CCA CTA CCA CAG CCA CAG ATG CAG CCA CAG TTT CAG Pro Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln 545 550 555 | | | 2218 |
| TTG CAG ATC CAG CCC CAG ATG CAG CTA CCA CAG CTG CTG CCG CAA CTG Leu Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu 560 565 570 575 | | | 2266 |
| CAA CCT CAG CAG CAG COT GAT CCT GAG CCA GAG CCA GAG CCA GAG CCA Gln Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro 580 585 590 | | | 2314 |
| GAG CCA GAG CCA GAG CCA GAG CCG GAA CCG GAA CCG GAG CCA GAG CCA Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro 595 600 605 | | | 2362 |
| GAG CCA GAA CCA GAG CCA GAG GAA GAA CAG GAA GAG GCA GAA GAA GAG Glu Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu 610 615 620 | | | 2410 |
| GCA GAG GAA GGA GCA GAG GAA GGA GCA GAA CCA GAG GCA CAG GCA GAA Ala Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu 625 630 635 | | | 2458 |
| GAA GAG GAA GAG GAA GAG GAA GCG GAA GAG CCA CAG CCA GAA GAA GCC Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala 640 645 650 655 | | | 2506 |
| CAA ATA GCA GGA CTC GTC TAT AAG AAA TGG ACA GTT TAG TTCCTCTTCT Gln Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val 660 665 | | | 2555 |
| TGTTAGCTTA CTCTGTAGTT TCTTCTTCTT GTTGCCCATTT GTGTAGCTTT ATAGAGTGTG | | | 2615 |

| | |
|---|------|
| ACGCTATTGA TGTCTCCATT TTTTAAAGTG AATTTAAATG TACTGTTCAA TATTTTTCAT | 2675 |
| GTGATGTTGT TCCAATGTGA GTTACGACTT CATTTATCTT AAAGACAAA CTGGTTGTCA | 2735 |
| GTCATATCTG ACAGAAGAAA GAAATCACTG TGTAACCAAG CCATATAGCG GCCGC | 2790 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 668 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Phe | Arg | Cys | Gln | Lys | Cys | Gly | Lys | Ser | Phe | Val | Thr | Leu | 1 | 5 | 10 | 15 |
| Glu | Lys | Phe | Thr | Ile | His | Asn | Tyr | Ser | His | Ser | Arg | Glu | Arg | Pro | Phe | 20 | 25 | 30 | |
| Lys | Cys | Ser | Lys | Ala | Glu | Cys | Gly | Lys | Ala | Phe | Val | Ser | Lys | Tyr | Lys | 35 | 40 | 45 | |
| Leu | Met | Arg | His | Met | Ala | Thr | His | Ser | Pro | Gln | Lys | Ile | His | Gln | Cys | 50 | 55 | 60 | |
| Thr | His | Cys | Glu | Lys | Thr | Phe | Asn | Arg | Lys | Asp | His | Leu | Lys | Asn | His | 65 | 70 | 75 | 80 |
| Leu | Gln | Thr | His | Asp | Pro | Asn | Lys | Ile | Ser | Tyr | Ala | Cys | Asp | Asp | Cys | 85 | 90 | 95 | |
| Gly | Lys | Lys | Tyr | His | Thr | Met | Leu | Gly | Tyr | Lys | Arg | His | Leu | Ala | Leu | 100 | 105 | 110 | |
| His | Ser | Ala | Ser | Asn | Gly | Asp | Leu | Thr | Cys | Gly | Val | Cys | Thr | Leu | Glu | 115 | 120 | 125 | |
| Leu | Gly | Ser | Thr | Glu | Val | Leu | Leu | Asp | His | Leu | Lys | Ser | His | Ala | Glu | 130 | 135 | 140 | |
| Glu | Lys | Ala | Asn | Gln | Ala | Pro | Arg | Glu | Lys | Lys | Tyr | Gln | Cys | Asp | His | 145 | 150 | 155 | 160 |
| Cys | Asp | Arg | Cys | Phe | Tyr | Thr | Arg | Lys | Asp | Val | Arg | Arg | His | Leu | Val | 165 | 170 | 175 | |
| Val | His | Thr | Gly | Cys | Lys | Asp | Phe | Leu | Cys | Gln | Phe | Cys | Ala | Gln | Arg | 180 | 185 | 190 | |
| Phe | Gly | Arg | Lys | Asp | His | Leu | Thr | Arg | His | Thr | Lys | Lys | Thr | His | Ser | 195 | 200 | 205 | |
| Gln | Glu | Leu | Met | Gln | Glu | Asn | Met | Gln | Ala | Gly | Asp | Tyr | Gln | Ser | Asn | | | | |

| 210 | 215 | 220 |
|--|-----|-----|
| Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro 225 230 235 240 | | |
| Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp Gly 245 250 255 | | |
| Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu Glu 260 265 270 | | |
| Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro 275 280 285 | | |
| Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro Leu 290 295 300 | | |
| Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln 305 310 315 320 | | |
| Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu Pro 325 330 335 | | |
| Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro Met 340 345 350 | | |
| Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met Leu 355 360 365 | | |
| Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro Glu 370 375 380 | | |
| Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro Pro 385 390 395 400 | | |
| Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr Ala 405 410 415 | | |
| Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys Asn 420 425 430 | | |
| Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro Leu 435 440 445 | | |
| Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys Val 450 455 460 | | |
| Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro 465 470 475 480 | | |
| Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro 485 490 495 | | |
| Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro 500 505 510 | | |
| Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln Pro 515 520 525 | | |

Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro
 530 535 540
 Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu
 545 550 555 560
 Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln
 565 570 575
 Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
 580 585 590
 Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
 595 600 605
 Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala
 610 615 620
 Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu
 625 630 635 640
 Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln
 645 650 655
 Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val *
 660 665

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGTCTCGAG GCCTTTGCGG CCGCTATANN NNNNNN

36

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGCCATGG

9

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "N at position 3 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCNCCATGG

9

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ser | Arg | Glu | Arg | Pro | Phe | Lys | Cys |
| 1 | | | | 5 | | | | |

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Cross-links
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "X at position 2 is S or T."

(ix) FEATURE:

- (A) NAME/KEY: Cross-links
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "X at position 7 is F or Y."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

His Xaa Gly Glu Lys Pro Xaa Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

His Ser Pro Gln Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Lys Lys Trp Thr
1

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotid",

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTGATGGCGG CCGCCATTCC GCTGTCAAAA ATGTG

35

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCGCGCCTCG AGGGTCTTCT TGGTGTGACG

30

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCGGCCGCAG AGCCGTCTTT CACTC

25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGCGCCTCG AGAACTGTCC ATTTCTTATA GAC

33

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATAGCAGTGA GTGCTGTG

18

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTTTCTTTTC AGGGACTC

18

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 803..2192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

| | |
|---|-----|
| CGGTTCTTTC AATTCAGAAT TTGTTTTAGG TTCTGTTATT GCATAGATTT GCATACCTGT | 60 |
| TTTATGGTAT TTTAATACTG TTGGTTTTAA AAAATACCAT TTCCTCTGAG TGCTGTTCTG | 120 |
| AATATATTAT GTAAGCAATT TTGTGTGTTT TTTTTTTTCC ACTTGCATAA AGCAGGGGAA | 180 |
| AAGTTGAGAG TTTTCTTAA TCCAGTCCCA AGTAGGACAA AGGATATGAG TGTTTAAAGA | 240 |
| TCATCTATTA AAATGCATGA AAAAACTA GAAATCTCC TGTGCACATC GCCAGTCGTG | 300 |
| TGTGTGCTCT AGAAGTGAAG TTCAGGGGGT AACATAATGG AGGAATGTTT TCCTAGCTTC | 360 |
| ATTCCCTGAC GATGTACAAG GTCTCTTCTC ACAGGTTTGA ATCTTCAGAC AAACCTCTGG | 420 |

| | |
|---|------|
| GAGGACTGGG AGGACTCGGT CCCTGCCTCG CAGCAGATGT TCCCTGTCAC TCAGTAGCCA | 480 |
| ATCCGGGGGA CCCAGGACAT GCCCCAGCTA TAGTGATGCA GATTACCTTT CTGGTCCTGA | 540 |
| ATCGCACCTG TGCCTCGAGA CTTTCTCCCC TCAGCTTGAG ACTGCATGTA AACTGGGATG | 600 |
| TGTGAAAGCA GGAAGCAAAG CTAGTGACAG CTGAGAGGTC CATGTCTGGG TAGAACCAGG | 660 |
| CCCACGATGC TGCCTCTCCC GTGGTCTGGA GTTCAGCTGC AGGGACTCTG CTGATTGGCC | 720 |
| CAGCACCATC GTTCTGTTTG TGCTTAAATG GCACAGCATT TGGTCAGCAC ATCTGAAAAG | 780 |
| GAAGGTGTGA GAAGCAAAGC CC ATG GCC ACG TTC CCC TGC CAG TTA TGT GGC | 832 |
| Met Ala Thr Phe Pro Cys Gln Leu Cys Gly | |
| 1 5 10 | |
| AAG ACG TTC CTC ACC CTG GAG AAG TTC ACG ATT CAC AAT TAT TCC CAC | 880 |
| Lys Thr Phe Leu Thr Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His | |
| 15 20 25 | |
| TCC AGG GAG CGG CCG TAC AAG TGT GTG CAG CCT GAC TGT GGC AAA GCC | 928 |
| Ser Arg Glu Arg Pro Tyr Lys Cys Val Gln Pro Asp Cys Gly Lys Ala | |
| 30 35 40 | |
| TTT GTT TCC AGA TAT AAA TTG ATG AGG CAT ATG GCT ACC CAT TCT CCC | 976 |
| Phe Val Ser Arg Tyr Lys Leu Met Arg His Met Ala Thr His Ser Pro | |
| 45 50 55 | |
| CAG AAA TCT CAC CAG TGT GCT CAC TGT GAG AAG ACG TTC AAC CGG AAA | 1024 |
| Gln Lys Ser His Gln Cys Ala His Cys Glu Lys Thr Phe Asn Arg Lys | |
| 60 65 70 | |
| GAC CAC CTG AAA AAC CAC CTC CAG ACC CAC GAC CCC AAC AAA ATG GCC | 1072 |
| Asp His Leu Lys Asn His Leu Gln Thr His Asp Pro Asn Lys Met Ala | |
| 75 80 85 90 | |
| TTT GGG TGT GAG GAG TGT GGG AAG AAG TAC AAC ACC ATG CTG GGC TAT | 1120 |
| Phe Gly Cys Glu Glu Cys Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr | |
| 95 100 105 | |
| AAG AGG CAC CTG GCC CTC CAT GCG GCC AGC AGT GGG GAC CTC ACC TGT | 1168 |
| Lys Arg His Leu Ala Leu His Ala Ala Ser Ser Gly Asp Leu Thr Cys | |
| 110 115 120 | |
| GGG GTC TGT GCC CTG GAG CTA GGG AGC ACC GAG GTG CTA CTG GAC CAC | 1216 |
| Gly Val Cys Ala Leu Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His | |
| 125 130 135 | |
| CTC AAA GCC CAT GCG GAA GAG AAG CCC CCT AGC GGA ACC AAG GAA AAG | 1264 |
| Leu Lys Ala His Ala Glu Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys | |
| 140 145 150 | |
| AAG CAC CAG TGC GAC CAC TGT GAA AGA TGC TTC TAC ACC CGG AAG GAT | 1312 |
| Lys His Gln Cys Asp His Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp | |
| 155 160 165 170 | |

| | |
|---|------|
| GTG CGA CGC CAC CTG GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGC Val Arg Arg His Leu Val Val His Thr Gly Cys Lys Asp Phe Leu Cys 175 180 185 | 1360 |
| CAG TTC TGT GCC CAG AGA TTT GGG CGC AAG GAT CAC CTC ACC CGG CAT Gln Phe Cys Ala Gln Arg Phe Gly Arg Lys Asp His Leu Thr Arg His 190 195 200 | 1408 |
| ACC AAG AAG ACC CAC TCA CAG GAG CTG ATG AAA GAG AGC TTG CAG ACC Thr Lys Lys Thr His Ser Gln Glu Leu Met Lys Glu Ser Leu Gln Thr 205 210 215 | 1456 |
| GGA GAC CTT CTG AGC ACC TTC CAC ACC ATC TCG CCT TCA TTC CAA CTG Gly Asp Leu Leu Ser Thr Phe His Thr Ile Ser Pro Ser Phe Gln Leu 220 225 230 | 1504 |
| AAG GCT GCT GCC TTG CCT CCT TTC CCT TTA GGA GCT TCT GCC CAG AAC Lys Ala Ala Ala Leu Pro Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn 235 240 245 250 | 1552 |
| GGG CTT GCA AGT AGC TTG CCA GCT GAG GTC CAT AGC CTC ACC CTC AGT Gly Leu Ala Ser Ser Leu Pro Ala Glu Val His Ser Leu Thr Leu Ser 255 260 265 | 1600 |
| CCC CCA GAA CAA GCC GCC CAG CCT ATG CAG CCG CTG CCA GAG TCC CTG Pro Pro Glu Gln Ala Ala Gln Pro Met Gln Pro Leu Pro Glu Ser Leu 270 275 280 | 1648 |
| GCC TCC CTC CAC CCC TCG GTA TCC CCT GGC TCT CCT CCG CCA CCC CTT Ala Ser Leu His Pro Ser Val Ser Pro Gly Ser Pro Pro Pro Pro Leu 285 290 295 | 1696 |
| CCC AAT CAC AAG TAC AAC ACC ACT TCT ACC TCA TAC TCC CCA CTT GCA Pro Asn His Lys Tyr Asn Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala 300 305 310 | 1744 |
| AGC CTG CCC CTC AAA GCA GAT ACT AAA GGT TTT TGC AAT ATC AGT TTG Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu 315 320 325 330 | 1792 |
| TTT GAG GAC TTG CCT CTG CAA GAG CCT CAG TCA CCT CAA AAG CTC AAC Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn 335 340 345 | 1840 |
| CCA GGT TTT GAT CTG GCT AAG GGA AAT GCT GGT AAA GTA AAC CTG CCC Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala Gly Lys Val Asn Leu Pro 350 355 360 | 1888 |
| AAG GAG CTG CCT GCA GAT GCT GTG AAC CTA ACA ATA CCT GCC TCT CTG Lys Glu Leu Pro Ala Asp Ala Val Asn Leu Thr Ile Pro Ala Ser Leu 365 370 375 | 1936 |
| GAC CTG TCC CCC CTG TTG GGC TTC TGG CAG CTG CCC CCT CCT GCT ACC Asp Leu Ser Pro Leu Leu Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr | 1984 |

| 380 | 395 | 390 | |
|--|-----|-----|------|
| CAA AAT ACC TTT GGG AAT AGC ACT CTT GCC CTG GGG CCT GGG GAA TCT | | | 2032 |
| Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser | | | |
| 395 | 400 | 405 | 410 |
| TTG CCC CAC AGG TTA AGC TGT CTG GGG CAG CAG CAG CAA GAA CCC CCA | | | 2080 |
| Leu Pro His Arg Leu Ser Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro | | | |
| | 415 | 420 | 425 |
| CTT GCC ATG GGC ACT GTG AGC CTG GGC CAG CTC CCC CTG CCC CCC ATC | | | 2128 |
| Leu Ala Met Gly Thr Val Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile | | | |
| | 430 | 435 | 440 |
| CCT CAT GTG TTC TCA GCT GGC ACT GGC TCT GCC ATC CTG CCT CAT TTC | | | 2176 |
| Pro His Val Phe Ser Ala Gly Thr Gly Ser Ala Ile Leu Pro His Phe | | | |
| | 445 | 450 | 455 |
| CAT CAT GCA TTC AGA T AATTGATTTT TAAAGTGTAT TTTTCGTATT | | | 2222 |
| His His Ala Phe Arg | | | |
| | 460 | | |
| CTGGAAGATG TTTTAAGAAG CATTTTAAAT GTCAGTACACA ATATGAGAAA GATTTGGAAA | | | 2282 |
| ACGAGACTGG GACTATGGCT TATTCAGTGA TGACTGGCTT GAGATGATAA GA | | | 2334 |

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Phe | Pro | Cys | Gln | Leu | Cys | Gly | Lys | Thr | Phe | Leu | Thr | Leu |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Glu | Lys | Phe | Thr | Ile | His | Asn | Tyr | Ser | His | Ser | Arg | Glu | Arg | Pro | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Cys | Val | Gln | Pro | Asp | Cys | Gly | Lys | Ala | Phe | Val | Ser | Arg | Tyr | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Met | Arg | His | Met | Ala | Thr | His | Ser | Pro | Gln | Lys | Ser | His | Gln | Cys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | His | Cys | Glu | Lys | Thr | Phe | Asn | Arg | Lys | Asp | His | Leu | Lys | Asn | His |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Gln | Thr | His | Asp | Pro | Asn | Lys | Met | Ala | Phe | Gly | Cys | Glu | Glu | Cys |
| | | | | 85 | | | | | 90 | | | | | 95 | |

Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu
 100 105 110

His Ala Ala Ser Ser Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu
 115 120 125

Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ala His Ala Glu
 130 135 140

Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys Lys His Gln Cys Asp His
 145 150 155 160

Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
 165 170 175

Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
 180 185 190

Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
 195 200 205

Gln Glu Leu Met Lys Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr
 210 215 220

Phe His Thr Ile Ser Pro Ser Phe Gln Leu Lys Ala Ala Ala Leu Pro
 225 230 235 240

Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu
 245 250 255

Pro Ala Glu Val His Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala
 260 265 270

Gln Pro Met Gln Pro Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser
 275 280 285

Val Ser Pro Gly Ser Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn
 290 295 300

Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala
 305 310 315 320

Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu
 325 330 335

Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala
 340 345 350

Lys Gly Asn Ala Gly Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp
 355 360 365

Ala Val Asn Leu Thr Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu
 370 375 380

Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn
385 390 395 400

Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser Leu Pro His Arg Leu Ser
405 410 415

Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro Leu Ala Met Gly Thr Val
420 425 430

Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile Pro His Val Phe Ser Ala
435 440 445

Gly Thr Gly Ser Ala Ile Leu Pro His Phe His His Ala Phe Arg
450 455 460

B'



Dkt. 52130-A-PCT-US/JPW/EMW

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Dietmar Spengler and Laurent Journot
Serial No. : 09/254,870 Examiner: C. Patterson
Filed : August 16, 1999 Group Art Unit: 1652
For : NUCLEIC ACID MOLECULES CODING FOR TUMOR
SUPPRESSOR PROTEINS AND METHODS FOR THEIR
ISOLATION

1185 Avenue of the Americas
New York, New York 10036
June 26, 2000

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the enclosed computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(f) has the same information which is submitted as the paper copy of the "Sequence Listing" attached hereto as **Exhibit B**.

Respectfully submitted,

Elizabeth M. Wieckowski
Elizabeth M. Wieckowski
Registration No. 42,226
Cooper & Dunham LLP
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New York, New York 10036
(212) 278-0400